

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Baltimore, David
Cheng, Genhong
Cleary, Aileen
Lederman, Seth
Ye, Zheng-sheng
- (ii) TITLE OF INVENTION: TRUNCATED CRAF1 INHIBITS CD40 SIGNALING
- (iii) NUMBER OF SEQUENCES: 5
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Cooper & Dunham, LLP
(B) STREET: 1185 Avenue of the Americas
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: USA
(F) ZIP: 10036
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: White, John P
(B) REGISTRATION NUMBER: 28,678
(C) REFERENCE/DOCKET NUMBER: 50659
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 566 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Glu	Ser	Ser	Lys	Lys	Met	Asp	Ala	Ala	Gly	Thr	Leu	Gln	Pro	Asn
1				5					10					15	
Pro	Pro	Leu	Lys	Leu	Gln	Pro	Asp	Arg	Gly	Ala	Gly	Ser	Val	Leu	Val
			20					25					30		
Pro	Glu	Gln	Gly	Gly	Tyr	Lys	Glu	Lys	Phe	Val	Lys	Thr	Val	Glu	Asp
			35				40					45			
Lys	Tyr	Lys	Cys	Glu	Lys	Cys	Arg	Leu	Val	Leu	Cys	Asn	Pro	Lys	Gln
	50					55					60				
Thr	Glu	Cys	Gly	His	Arg	Phe	Cys	Glu	Ser	Cys	Met	Ala	Ala	Leu	Leu
65					70					75					80
Ser	Ser	Ser	Ser	Pro	Lys	Cys	Thr	Ala	Cys	Gln	Glu	Ser	Ile	Ile	Lys
				85					90					95	
Asp	Lys	Val	Phe	Lys	Asp	Asn	Cys	Cys	Lys	Arg	Glu	Ile	Leu	Ala	Leu
			100					105					110		
Gln	Val	Tyr	Cys	Arg	Asn	Glu	Gly	Arg	Gly	Cys	Ala	Glu	Gln	Leu	Thr
			115				120					125			
Leu	Gly	His	Leu	Leu	Val	His	Leu	Lys	Asn	Glu	Cys	Gln	Phe	Glu	Glu
	130					135					140				
Leu	Pro	Cys	Leu	Arg	Ala	Asp	Cys	Lys	Glu	Lys	Val	Leu	Arg	Lys	Asp
145					150					155					160
Leu	Arg	Asp	His	Val	Glu	Lys	Ala	Cys	Lys	Tyr	Arg	Glu	Ala	Thr	Cys
				165					170					175	
Ser	His	Cys	Lys	Ser	Gln	Val	Pro	Met	Ile	Lys	Leu	Gln	Lys	His	Glu
			180					185					190		
Asp	Thr	Asp	Cys	Pro	Cys	Val	Val	Val	Ser	Cys	Pro	His	Lys	Cys	Ser
		195					200					205			
Val	Gln	Thr	Leu	Leu	Arg	Ser	Glu	Leu	Ser	Ala	His	Leu	Ser	Glu	Cys
	210					215					220				
Val	Asn	Ala	Pro	Ser	Thr	Cys	Ser	Phe	Lys	Arg	Tyr	Gly	Cys	Val	Phe
225					230					235					240
Gln	Gly	Thr	Asn	Gln	Gln	Ile	Lys	Ala	His	Glu	Ala	Ser	Ser	Ala	Val
				245					250					255	
Gln	His	Val	Asn	Leu	Leu	Lys	Glu	Trp	Ser	Asn	Ser	Leu	Glu	Lys	Lys
			260					265					270		
Val	Ser	Leu	Leu	Gln	Asn	Glu	Ser	Val	Glu	Lys	Asn	Lys	Ser	Ile	Gln
		275					280					285			
Ser	Leu	His	Asn	Gln	Ile	Cys	Ser	Phe	Glu	Ile	Glu	Ile	Glu	Arg	Gln

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290	295	300
Lys Glu Met Leu	Arg Asn Asn Glu Ser Lys	Ile Leu His Leu Gln Arg
305	310	315 320
Val Ile Asp Ser	Gln Ala Glu Lys Leu	Lys Glu Leu Asp Lys Glu Ile
	325	330 335
Arg Pro Phe Arg	Gln Asn Trp Glu Glu Ala Asp Ser Met Lys Ser Ser	
	340	345 350
Val Glu Ser Leu	Gln Asn Arg Val Thr Glu Leu Glu Ser Val Asp Lys	
	355	360 365
Ser Ala Gly Gln	Ala Ala Arg Asn Thr Gly Leu Leu Glu Ser Gln Leu	
	370	375 380
Ser Arg His Asp	Gln Thr Leu Ser Val His Asp Ile Arg Leu Ala Asp	
	385	390 395 400
Met Asp Leu Arg	Phe Gln Val Leu Glu Thr Ala Ser Tyr Asn Gly Val	
	405	410 415
Leu Ile Trp Lys	Ile Arg Asp Tyr Lys Arg Arg Lys Gln Glu Ala Val	
	420	425 430
Met Gly Lys Thr	Leu Ser Leu Tyr Ser Gln Pro Phe Tyr Thr Gly Tyr	
	435	440 445
Phe Gly Tyr Lys	Met Cys Ala Arg Val Tyr Leu Asn Gly Asp Gly Met	
	450	455 460
Gly Lys Gly Thr	His Leu Ser Leu Phe Phe Val Ile Met Arg Gly Glu	
	465	470 475 480
Tyr Asp Ala Leu	Leu Pro Trp Pro Phe Lys Gln Lys Val Thr Leu Met	
	485	490 495
Leu Met Asp Gln	Gly Ser Ser Arg Arg His Leu Gly Asp Ala Phe Lys	
	500	505 510
Pro Asp Pro Asn	Ser Ser Ser Phe Lys Lys Pro Thr Gly Glu Met Asn	
	515	520 525
Ile Ala Ser Gly	Cys Pro Val Phe Val Ala Gln Thr Val Leu Glu Asn	
	530	535 540
Gly Thr Tyr Ile	Lys Asp Asp Thr Ile Phe Ile Lys Val Ile Val Asp	
	545	550 555 560
Thr Ser Asp Leu	Pro Asp	
	565	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 568 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met 1	Glu	Ser	Ser	Lys 5	Lys	Met	Asp	Ser	Pro 10	Gly	Ala	Leu	Gln	Thr	Asn 15
Pro	Pro	Leu	Lys 20	Leu	His	Thr	Asp	Arg 25	Ser	Ala	Gly	Thr	Pro 30	Val	Phe
Val	Pro	Glu 35	Gln	Gly	Gly	Tyr	Lys 40	Glu	Lys	Phe	Val	Lys 45	Thr	Val	Glu
Asp	Lys 50	Tyr	Lys	Cys	Glu	Lys 55	Cys	His	Leu	Val	Leu 60	Cys	Ser	Pro	Lys
Gln 65	Thr	Glu	Cys	Gly	His 70	Arg	Phe	Cys	Glu	Ser 75	Cys	Met	Ala	Ala	Leu 80
Leu	Ser	Ser	Ser	Ser 85	Pro	Lys	Cys	Thr	Ala 90	Cys	Gln	Glu	Ser	Ile 95	Val
Lys	Asp	Lys	Val 100	Phe	Lys	Asp	Asn 105	Cys	Cys	Lys	Arg	Glu 110	Ile	Leu	Ala
Leu	Gln 115	Ile	Tyr	Cys	Arg	Asn 120	Glu	Ser	Arg	Gly	Cys	Ala 125	Glu	Gln	Leu
Thr 130	Leu	Gly	His	Leu	Leu 135	Val	His	Leu	Lys	Asn 140	Asp	Cys	His	Phe	Glu
Glu 145	Leu	Pro	Cys	Val	Arg 150	Pro	Asp	Cys	Lys	Glu 155	Lys	Val	Leu	Arg	Lys 160
Asp	Leu	Arg	Asp	His 165	Val	Glu	Lys	Ala 170	Cys	Lys	Tyr	Arg	Glu 175	Ala	Thr
Cys	Ser	His	Cys 180	Lys	Ser	Gln	Val	Pro 185	Met	Ile	Ala	Leu	Gln 190	Lys	His
Glu	Asp	Thr 195	Asp	Cys	Pro	Cys	Val 200	Val	Val	Ser	Cys	Pro 205	His	Lys	Cys
Ser 210	Val	Gln	Thr	Leu	Leu	Arg 215	Ser	Glu	Leu	Ser	Ala 220	His	Leu	Ser	Glu
Cys 225	Val	Asn	Ala	Pro	Ser 230	Thr	Cys	Ser	Phe	Lys 235	Arg	Tyr	Gly	Cys	Val 240

Phe Gln Gly Thr Asn	Gln Gln Ile Lys Ala His Glu Ala Ser Ser Ala
245	250 255
Val Gln His Val Asn	Leu Leu Lys Glu Trp Ser Asn Ser Leu Glu Lys
260	265 270
Lys Val Ser Leu Leu	Gln Asn Glu Ser Val Glu Lys Asn Lys Ser Ile
275	280 285
Gln Ser Leu His Asn	Gln Ile Cys Ser Phe Glu Ile Glu Ile Glu Arg
290	295 300
Gln Lys Glu Met Leu	Arg Asn Asn Glu Ser Lys Ile Leu His Leu Gln
305	310 315 320
Arg Val Ile Asp Ser	Gln Ala Glu Lys Leu Lys Glu Leu Asp Lys Glu
325	330 335
Ile Arg Pro Phe Arg	Gln Asn Trp Glu Glu Ala Asp Ser Met Lys Ser
340	345 350
Ser Val Glu Ser Leu	Gln Asn Arg Val Thr Glu Leu Glu Ser Val Asp
355	360 365
Lys Ser Ala Gly Gln	Val Ala Arg Asn Thr Gly Leu Leu Glu Ser Gln
370	375 380
Leu Ser Arg His Asp	Gln Met Leu Ser Val His Asp Ile Arg Leu Ala
385	390 395 400
Asp Met Asp Leu Arg	Phe Gln Val Leu Glu Thr Ala Ser Tyr Asn Gly
405	410 415
Val Leu Ile Trp Lys	Ile Arg Asp Tyr Lys Arg Arg Lys Gln Glu Ala
420	425 430
Val Met Gly Lys Thr	Leu Ser Leu Tyr Ser Gln Pro Phe Tyr Thr Gly
435	440 445
Tyr Phe Gly Tyr Lys	Met Cys Ala Arg Val Tyr Leu Asn Gly Asp Gly
450	455 460
Met Gly Lys Gly Thr	His Leu Ser Leu Phe Phe Val Ile Met Arg Gly
465	470 475 480
Glu Tyr Asp Ala Leu	Leu Pro Trp Pro Phe Lys Gln Lys Val Thr Leu
485	490 495
Met Leu Met Asp Gln	Gly Ser Ser Arg Arg His Leu Gly Asp Ala Phe
500	505 510
Lys Pro Asp Pro Asn	Ser Ser Ser Phe Lys Lys Pro Thr Gly Glu Met
515	520 525
Asn Ile Ala Ser Gly	Cys Pro Val Phe Val Ala Gln Thr Val Leu Glu
530	535 540
Asn Gly Thr Tyr Ile	Lys Asp Asp Thr Ile Phe Ile Lys Val Ile Val

545

550

555

560

Asp Thr Ser Asp Leu Pro Asp Pro
565

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2359 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGCGGCGGAG GATGCGCGCG GCGCCTGAGC CGGCCGAACG GGCGGCCTCG GGGTACAGGG	60
TCCCCATTAC TTGAAGGATA AGGCTGGCAC GGCTCCGACG TCTGTGTGGA AGCTTCTCCC	120
TCCCTTCTGA GCTTCTCTAG ACTCCTTACA GCGCACGGCA CAGAATTTCA GTTTCCTAAG	180
ATGGAGTCAA GCAAAAAGAT GGATGCTGCT GGCACACTGC AGCCTAACCC ACCCCTAAAG	240
CTGCAGCCTG ATCGCGGCGC AGGGTCCGTG CTCGTGCCGG AGCAAGGAGG CTACAAGGAG	300
AAGTTTGTGA AGACGGTGGA AGACAAGTAC AAGTGCGAGA AGTGCCGCCT GGTGCTGTGC	360
AACCCGAAGC AGACGGAGTG TGGCCACCGG TTCTGCGAGA GCTGCATGGC CGCCCTGCTG	420
AGCTCCTCCA GTCCAAAATG CACAGCGTGC CAAGAAAGCA TCATCAAAGA CAAGGTGTTT	480
AAGGATAATT GCTGCAAGAG AGAGATTCTG GCCCTTCAGG TCTACTGTCG GAATGAAGGC	540
AGAGGTTGTG CGGAGCAGCT GACTCTGGGA CATCTGCTGG TGCACCTAAA AAATGAATGT	600
CAGTTTGAGG AACTTCCCTG TCTGCGTGCC GACTGCAAAG AAAAAGTACT GAGAAAAGAC	660
TTGCGGGATC ACGTGAAAA GGCCTGTAAA TACCGCGAGG CCACGTGCAG TCACTGCAAG	720
AGCCAAGTGC CCATGATCAA ACTGCAGAAA CATGAAGACA CAGATTGTCC CTGTGTGGTG	780
GTATCCTGCC CTCACAAGTG CAGCGTTCAG ACTCTTCTAA GGAGTGAGTT GAGTGCACAC	840
TTGTCCGAGT GTGTCAATGC CCCCAGCACC TGTAGTTTAA AGCGCTATGG CTGCGTTTTT	900
CAGGGTACAA ACCAGCAGAT CAAGGCCCAT GAGGCCAGCT CCGCGGTACA GCACGTGAAC	960
CTGCTGAAGG AGTGGAGCAA CTCCCTGGAG AAGAAGGTTT CCCTGCTGCA GAATGAAAGT	1020
GTTGAGAAAA ACAAGAGCAT CCAAAGCCTG CACAACCAGA TCTGCAGCTT TGAGATCGAG	1080
ATTGAGAGGC AGAAGGAGAT GCTCCGAAAC AACGAGTCCA AGATCCTTCA CCTGCAGCGG	1140

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C1

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(A) LENGTH: 2455 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGGGGAGCG CGGCGCGGCC GCGCGTGCG CGAGCCGGGG TTGCAGCCCA GCCGGGACTT 60

TCCAGCCGGC	GGCAGCCGGC	GCGGTCGTCTG	GCTCTTCCCC	GCCCCCGTC	ATGGGGCAGC	120
CCGGGGAGCA	GAACGCTGCG	GACCGCGGCG	GAGGACGCGC	CCGGCGCCCC	TGAGCCGGCC	180
GAGCGGCGAC	GGACCGCGAG	AACTCCTCTT	TCCTAAAATG	GAGTCGAGTA	AAAAGATGGA	240
CTCTCCTGGC	GCGCTGCAGA	CTAACCCGCC	GCTAAAGCTG	CACACTGACC	GTAGTGCTGG	300
GACGCCAGTT	TTTGTCCCTG	AACAAGGAGG	TTACAAGGAA	AAGTTTGTGA	AGACCGTGGA	360
GGACAAGTAC	AAGTGTGAGA	AGTGCCACCT	GGTGCTGTGC	AGCCCGAAGC	AGACCGAGTG	420
TGGGCACCGC	TTCTGCGAGA	GCTGCATGGC	GGCCCTGCTG	AGCTCTTCAA	GTCCAAAATG	480
TACAGCGTGT	CAAGAGAGCA	TCGTTAAGA	TAAGGTGTTT	AAGGATAATT	GCTGCAAGAG	540
AGAAATTCTG	GCTCTTCAGA	TCTATTGTCG	GAATGAAAGC	AGAGGTTGTG	CAGAGCAGTT	600
AACGCTGGGA	CATCTGCTGG	TGCATTTAAA	AAATGATTGC	CATTTTGAAG	AACTTCCATG	660
TGTGCGTCTT	GACTGCAAAG	AAAAGGTCTT	GAGGAAAGAC	CTGCGAGACC	ACGTGGAGAA	720
GGCGTGTA	TACCGGGAAG	CCACATGCAG	CCACTGCAAG	AGTCAGGTTT	CGATGATCGC	780
GCTGCAGAAA	CACGAAGACA	CCGACTGTCC	CTGCGTGGTG	GTGTCTTGCC	CTCACAAGTG	840
CAGCGTCCAG	ACTCTCCTGA	GGAGCGAGTT	GAGTGCACAC	TTGTCAGAGT	GTGTCAATGC	900
CCCCAGCACC	TGTAGTTTTA	AGCGCTATGG	CTGCGTTTTT	CAGGGGACAA	ACCAGCAGAT	960
CAAGGCCAC	GAGGCCAGCT	CCGCCGTGCA	GCACGTCAAC	CTGCTGAAGG	AGTGGAGCAA	1020
CTCGCTCGAA	AAGAAGGTTT	CCTTGTTGCA	GAATGAAAGT	GTAAGAAAAA	ACAAGAGCAT	1080
ACAAAGTTTG	CACAATCAGA	TATGTAGCTT	TGAAATTGAA	ATTGAGAGAC	AAAAGGAAAT	1140
GCTTCGAAAT	AATGAATCCA	AAATCCTTCA	TTACAGCGA	GTGATCGACA	GCCAAGCAGA	1200
GAAACTGAAG	GAGCTTGACA	AGGAGATCCG	GCCCTTCCGG	CAGAACTGGG	AGGAAGCAGA	1260
CAGCATGAAG	AGCAGCGTGG	AGTCCCTCCA	GAACCGCGTG	ACCGAGCTGG	AGAGCGTGGA	1320
CAAGAGTGCG	GGGCAAGTGG	CTCGGAACAC	AGGCCTGCTG	GAGTCCCAGC	TGAGCCGGCA	1380
TGACCAGATG	CTGAGTGTGC	ACGACATCCG	CCTAGCCGAC	ATGGACCTGC	GCTTCCAGGT	1440
CCTGGAGACC	GCCAGCTACA	ATGGAGTGCT	CATCTGGAAG	ATTCGCGACT	ACAAGCGGCG	1500
GAAGCAGGAG	GCCGTCATGG	GGAAGACCCT	GTCCCTTTAC	AGCCAGCCTT	TCTACACTGG	1560
TTACTTTGGT	TATAAGATGT	GTGCCAGGGT	CTACCTGAAC	GGGGACGGGA	TGGGGAAGGG	1620
GACGCACTTG	TCGCTGTTTT	TTGTCAATCAT	GCGTGAGAGAA	TATGATGCCC	TGCTTCCTTG	1680
GCCGTTTAAAG	CAGAAAGTGA	CACTCATGCT	GATGGATCAG	GGGTCCTCTC	GACGTCATTT	1740
GGGAGATGCA	TTCAAGCCCG	ACCCCAACAG	CAGCAGCTTC	AAGAAGCCCA	CTGGAGAGAT	1800

-C1

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Lys Ala Cys | Lys Tyr Arg
1 5